

**Figure 1 : Alignment of the BASB040 polynucleotide sequences. Identity to SeqID No:1 is indicated by a dot.**

		*	20	*	
Seqid1	:	ATGATGATCAAACCGACCGCCCTGCTCCTG	:	30	
Seqid3	:	.....	:	30	
Seqid5	:		:	-	
		40	*	60	
Seqid1	:	CCGGCTTTATTTTCTTTCCGCACGCATAC	:	60	
Seqid3	:	.....	:	60	
Seqid5	:		:	-	
		*	80	*	
Seqid1	:	GCGCCTGCCGCCGACCTTTCCGAAAACAAG	:	90	
Seqid3	:	.....	:	90	
Seqid5	:	.....	:	24	
		100	*	120	
Seqid1	:	GCGGCGGGTTTCGCATTGTTCAAAAACAAA	:	120	
Seqid3	:	.....	:	120	
Seqid5	:	.....	:	54	
		*	140	*	
Seqid1	:	AGCCCCGACACCGAATCAGTTAAATTAAAA	:	150	
Seqid3	:	.....	:	150	
Seqid5	:	.....C.....	:	84	
		160	*	180	
Seqid1	:	CCCAAATTCCCCGTCCGCATCGACACGCAG	:	180	
Seqid3	:	.....	:	180	
Seqid5	:	.....T.....	:	114	

\*                      200                      \*

Seqid1 : GATAGTGAAATCAAAGATATGGTCGAAGAA : 210  
Seqid3 : ..... : 210  
Seqid5 : ..C..... : 144

220                      \*                      240

Seqid1 : CACCTGCCGCTCATCACGCAGCAGCAGGAA : 240  
Seqid3 : ..... : 240  
Seqid5 : ..... : 174

\*                      260                      \*

Seqid1 : GAAGTATTGGACAAGGAACAGACGGGCTTC : 270  
Seqid3 : ..... : 270  
Seqid5 : ..... : 204

280                      \*                      300

Seqid1 : CTCGCCGAAGAAGCACCGGACAACGTTAAA : 300  
Seqid3 : ..... : 300  
Seqid5 : .....G..... : 234

\*                      320                      \*

Seqid1 : ACCATGCTCCGCAGCAAAGGCTATTTTCAGC : 330  
Seqid3 : ..... : 330  
Seqid5 : ..G..... : 264

340                      \*                      360

Seqid1 : AGCAAAGTCAGCCTGACGGAAAAAGACGGA : 360  
Seqid3 : ..... : 360  
Seqid5 : ..... : 294

\*                      380                      \*

Seqid1 : GCTTATACGGTACACATCACACCGGGCCCG : 390  
Seqid3 : ..... : 390  
Seqid5 : ..... : 324

400 \* 420  
Seqid1 : CGCACCAAATCGCCAACGTCGGTGTCGCC : 420  
Seqid3 : ..... : 420  
Seqid5 : .....C..... : 354

\* 440 \*  
Seqid1 : ATCCTCGGCGACATCCTTTCAGACGGCAAC : 450  
Seqid3 : ..... : 450  
Seqid5 : ..... : 384

460 \* 480  
Seqid1 : CTCGCCGAATACTACCGCAACGCGCTGGAA : 480  
Seqid3 : ..... : 480  
Seqid5 : ..... : 414

\* 500 \*  
Seqid1 : AACTGGCAGCAGCCGGTAGGCAGTGATTTC : 510  
Seqid3 : ..... : 510  
Seqid5 : .....C..... : 444

520 \* 540  
Seqid1 : GATCAGGACAGTTGGGAAAACAGCAAAACT : 540  
Seqid3 : ..... : 540  
Seqid5 : ..... : 474

\* 560 \*  
Seqid1 : TCCGTCCTCGGCGCGGTAAACGCGAAAAGGC : 570  
Seqid3 : .....C..... : 570

Seqid5 : .....C....C. : 504

Seqid1 : TACCCGCTTGCCAAGCTCGGCAACACCCGG : 600  
Seqid3 : ..... : 600  
Seqid5 : .....T..G.A. : 534

Seqid1 : GCGGCCGTCAACCCCGATAACCGCCACCGTC : 630  
Seqid3 : ..... : 630  
Seqid5 : .....C. : 564

Seqid1 : GATTTGAACGTCGTCGTGGACAGCGGCCGC : 660  
Seqid3 : ..... : 660  
Seqid5 : ..... : 594

Seqid1 : CCCATCGCCTTCGGCGACTTTGAAATCACC : 690  
Seqid3 : ..... : 690  
Seqid5 : ..... : 624

Seqid1 : GGCACACAGCGTTACCCCGAACAAATCGTC : 720  
Seqid3 : ..... : 720  
Seqid5 : ..... : 654

Seqid1 : TCCGGCCTGGCGCGCTTCCAACCGGGCACG : 750  
Seqid3 : ..... : 750  
Seqid5 : .....T.....T.....G..C..T.T. : 684

760 \* 780  
Seqid1 : CCCTACGACCTCGACCTGCTGCTCGACTTC : 780  
Seqid3 : ..... : 780  
Seqid5 : ..G..... : 714

\* 800 \*  
Seqid1 : CAACAGGCACTCGAACAAAACGGGCATTAT : 810  
Seqid3 : ..... : 810  
Seqid5 : .....G..... : 744

820 \* 840  
Seqid1 : TCCGGCGCGTCCGTACAAGCCGACTTCGAC : 840  
Seqid3 : ..... : 840  
Seqid5 : ..... : 774

\* 860 \*  
Seqid1 : CGTCTCCAAGGCGACCGCGTCCCCGTCAA : 870  
Seqid3 : ..... : 870  
Seqid5 : ..C..... : 804

880 \* 900  
Seqid1 : GTCAGCGTAACCGAGGTCAAACGCCACAAG : 900  
Seqid3 : ..... : 900  
Seqid5 : .....A : 834

\* 920 \*  
Seqid1 : CTCGAAACCGGCATCCGCCTCGATTTCGGAA : 930  
Seqid3 : ..... : 930  
Seqid5 : ..... : 864

940 \* 960  
Seqid1 : TACGGTTTGGGCGGCAAAATCGCCTACGAC : 960

Seqid3 : ..... : 960  
Seqid5 : ..... : 894

                  \*          980          \*  
Seqid1 : TATTACAACCTCTTCAACAAAGGCTATATC : 990  
Seqid3 : ..... : 990  
Seqid5 : ..... : 924

                  1000          \*          1020  
Seqid1 : GGCTCGGTCGTCTGGGATATGGACAAATAC : 1020  
Seqid3 : ..... : 1020  
Seqid5 : ..T..... : 954

                  \*          1040          \*  
Seqid1 : GAAACCACGCTTGCCGCCGGCATCAGCCAG : 1050  
Seqid3 : ..... : 1050  
Seqid5 : ..... : 984

                  1060          \*          1080  
Seqid1 : CCGCGCAACTATCGGGGCAACTACTGGACA : 1080  
Seqid3 : ..... : 1080  
Seqid5 : ..... : 1014

                  \*          1100          \*  
Seqid1 : AGCAACGTTTCTCTACAACCGTTCGACCACC : 1110  
Seqid3 : ..... : 1110  
Seqid5 : ..... : 1044

                  1120          \*          1140  
Seqid1 : CAAAACCTCGAAAAACGCGCCTTCTCCGGC : 1140  
Seqid3 : ..... : 1140  
Seqid5 : ..... : 1074

\*                    1160                    \*

Seqid1 : GGCATCTGGTATGTGCGCGACCGCGCGGGC : 1170  
Seqid3 : ..... : 1170  
Seqid5 : ...G..... : 1104

1180                    \*                    1200

Seqid1 : ATCGATGCCAGGCTGGGGGCAGAGTTTCTC : 1200  
Seqid3 : ..... : 1200  
Seqid5 : .....G..A..... : 1134

\*                    1220                    \*

Seqid1 : GCAGAAGGCCGGAAAATCCCCGGCTCGGAT : 1230  
Seqid3 : ..... : 1230  
Seqid5 : .....C. : 1164

1240                    \*                    1260

Seqid1 : ATCGATTTGGGCAACAGCCACGCCACGATG : 1260  
Seqid3 : ..... : 1260  
Seqid5 : G..... : 1194

\*                    1280                    \*

Seqid1 : CTGACCGCCTCTTGGAACGCCAGCTGCTC : 1290  
Seqid3 : ..... : 1290  
Seqid5 : ..... : 1224

1300                    \*                    1320

Seqid1 : AACCAACGTGCTGCATCCCGAAAACGGCCAT : 1320  
Seqid3 : ..... : 1320  
Seqid5 : ..... : 1254

\*                    1340                    \*

Seqid1 : TACCTCGACGGCAAAATCGGTACGACTTTG : 1350  
Seqid3 : ..... : 1350  
Seqid5 : ..... : 1284

1360 \* 1380  
Seqid1 : GGCACATTCCTGTCCTCCACCGCGCTGATC : 1380  
Seqid3 : ..... : 1380  
Seqid5 : ..... : 1314

\* 1400 \*  
Seqid1 : CGCACCTCTGCCCCGTGCAGGTTATTTCTTC : 1410  
Seqid3 : ..... : 1410  
Seqid5 : ..... : 1344

1420 \* 1440  
Seqid1 : ACGCCCGAAAACAAAAAACTCGGCACGTTC : 1440  
Seqid3 : ..... : 1440  
Seqid5 : ..... : 1374

\* 1460 \*  
Seqid1 : ATCATACGCGGACAAGCGGGTTACACCGTT : 1470  
Seqid3 : ..... : 1470  
Seqid5 : ..... : 1404

1480 \* 1500  
Seqid1 : GCCCGCGACAATGCCGACGTTCCTTCAGGG : 1500  
Seqid3 : ..... : 1500  
Seqid5 : ..... : 1434

\* 1520 \*  
Seqid1 : CTGATGTTCCGCAGCGGCGGCGGTCTTCC : 1530  
Seqid3 : ..... : 1530



Seqid5 : ..... : 1464

                  1540                  \*                  1560  
Seqid1 : GTGCGCGGTTACGAACTCGACAGCATCGGA : 1560  
Seqid3 : ..... : 1560  
Seqid5 : ..... : 1494

                                  \*                  1580                  \*  
Seqid1 : CTTGCCGGCCCCGAACGGATCGGTCCTGCCC : 1590  
Seqid3 : ..... : 1590  
Seqid5 : ..... : 1524

                  1600                  \*                  1620  
Seqid1 : GAACGCGCCCTCCTGGTGGGCAGCCTGGAA : 1620  
Seqid3 : ..... : 1620  
Seqid5 : ..... : 1554

                                  \*                  1640                  \*  
Seqid1 : TACCAACTGCCGTTTACGCGCACCCCTTTCC : 1650  
Seqid3 : ..... : 1650  
Seqid5 : ..... : 1584

                  1660                  \*                  1680  
Seqid1 : GGCGCGGTGTTCCACGATATGGGCGATGCC : 1680  
Seqid3 : ..... : 1680  
Seqid5 : ..... : 1614

                                  \*                  1700                  \*  
Seqid1 : GCCGCCAATTTCAAACGTATGAAGCTGAAA : 1710  
Seqid3 : ..... : 1710  
Seqid5 : ..... : 1644

1720 \* 1740  
Seqid1 : CACGGTTCGGGACTGGGCGTGCGCTGGTTC : 1740  
Seqid3 : ..... : 1740  
Seqid5 : ..... : 1674

\* 1760 \*  
Seqid1 : AGCCCGCTTGCGCCGTTTTCCTTCGACATC : 1770  
Seqid3 : ..... : 1770  
Seqid5 : ..... : 1704

1780 \* 1800  
Seqid1 : GCCTACGGGCACAGCGATAAGAAAATCCGC : 1800  
Seqid3 : ..... : 1800  
Seqid5 : ..... : 1734

\* 1820 \*  
Seqid1 : TGGCACATCAGCTTGGGAACACGCTTCTAA : 1830  
Seqid3 : ..... : 1830  
Seqid5 : ..... : 1764

**Figure 2 : Alignment of the BASB040 polypeptide sequences.**  
Identity to SeqID No:2 is indicated by a dot.

	*	20	*
Seqid2	:	MMIKPTALLLPALFFFPAYAPAADLSENK	: 30
Seqid4	:	.....	: 30
Seqid6	:	.....	: 8
	40	*	60
Seqid2	:	AAGFALFKNKSPDTESVKLKPKFPVRIDTQ	: 60
Seqid4	:	.....	: 60
Seqid6	:	.....L.....	: 38
	*	80	*
Seqid2	:	DSEIKDMVEEHLPLITQQQEEVLDKEQTGF	: 90
Seqid4	:	.....	: 90
Seqid6	:	.....	: 68
	100	*	120
Seqid2	:	LAEEAPDENVKTMRLRSKGYFSSKVSLTEKDG	: 120
Seqid4	:	.....	: 120
Seqid6	:	.....	: 98

\* 140 \*

Seqid2 : AYT VHITPGPRTKIANVGVA ILGDILSDGN : 150  
Seqid4 : ..... : 150  
Seqid6 : ..... : 128

160 \* 180

Seqid2 : LAEYYRNALENWQQPVGSDFDQDSWENSKT : 180  
Seqid4 : ..... : 180  
Seqid6 : ..... : 158

\* 200 \*

Seqid2 : SVLGAVTRKGYPLAKLGNTAAVNPDTATV : 210  
Seqid4 : ..... : 210  
Seqid6 : .....A.....Q.....A : 188

220 \* 240

Seqid2 : DLNVVVDSGRPIAFGDFEITGTQRYPEQIV : 240  
Seqid4 : ..... : 240  
Seqid6 : ..... : 218

\* 260 \*

Seqid2 : SGLARFQPGTPYDLDLLLDFQQALEQNGHY : 270  
Seqid4 : ..... : 270  
Seqid6 : .....M..... : 248

280 \* 300

Seqid2 : SGASVQADFDRLOGDRVPVKVSVTEVKRHK : 300  
Seqid4 : ..... : 300  
Seqid6 : ..... : 278

\* 320 \*

Seqid2 : LETGIRLDSEYGLGGKIAVDYYNLFNKGYYI : 330  
Seqid4 : ..... : 330  
Seqid6 : ..... : 308

340 \* 360

Seqid2 : GSVVWMDMDKYETTLAAGISQPRNYRGNYWT : 360  
Seqid4 : ..... : 360  
Seqid6 : ..... : 338

\* 380 \*

Seqid2 : SNVSYNRSTTQNLEKRAFSGGIWYVRDRAG : 390  
Seqid4 : ..... : 390

Seqid6 : ..... : 368

400 \* 420

Seqid2 : IDARLGAEFLAEGRKIPGSDIDLGNSHATM : 420

Seqid4 : ..... : 420

Seqid6 : .....A..... : 398

\* 440 \*

Seqid2 : LTASWKRQLLNVLHPENGHYLDGKIGTTL : 450

Seqid4 : ..... : 450

Seqid6 : ..... : 428

460 \* 480

Seqid2 : GTFLSSTALIRTSARAGYFFTPENKKLGTF : 480

Seqid4 : ..... : 480

Seqid6 : ..... : 458

\* 500 \*

Seqid2 : IIRGQAGYTVARDNADVPSGLMFRSGGASS : 510

Seqid4 : ..... : 510

Seqid6 : ..... : 488

520 \* 540  
Seqid2 : VRGYELDSIGLAGPNGSVLPERALLVGSLE : 540  
Seqid4 : ..... : 540  
Seqid6 : ..... : 518

\* 560 \*  
Seqid2 : YQLPFTRTLGAVFHDMDAAANFKRMKLK : 570  
Seqid4 : ..... : 570  
Seqid6 : ..... : 548

580 \* 600  
Seqid2 : HGSGLGVRWFSPLAPFSFDIAYGHSDKKIR : 600  
Seqid4 : ..... : 600  
Seqid6 : ..... : 578

Seqid2 : WHISLGTRF : 609  
Seqid4 : ..... : 609  
Seqid6 : ..... : 587

## SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel compounds

<130> BM45339

<160> 11

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1830

<212> DNA

<213> *Neisseria meningitidis*

<400> 1

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agccccgaca ccgaatcagt taaattaaaa cccaaattcc ccgtccgcat cgacacgcag	180
gatagtgaat tcaaagatat ggtcgaagaa cacctgccgc tcatcacgca gcagcaggaa	240
gaagtattgg acaaggaaca gacgggcttc ctgcgcgaag aagcacgcga caacgttaaa	300
accatgctcc gcagcaaaagg ctatttcagc agcaaaagtc gcctgacgga aaaagacgga	360
gcttatacgg tacacatcac accgggcccc cgacacaaaa tcgccaacgt cgggtgctgcc	420
atcctcggcg acatcctttc agacggcaac ctgcgcgaat actaccgca cgcgctggaa	480
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tccgtcctcg gcgcggtaac gcgaaaaggc taccgccttg ccaagctcgg caacacccgg	600
gcggccgtca accccgatac cgccaccgtc gatttgaaac tcgtcgtgga cagcggccgc	660
cccatcgcct tcggcgactt tgaaatcacc ggcacacagc gttaccccg acaaatcgtc	720
tccggcctgg cgcgcttcca accgggcacg ccctacgacc tcgacctgct gctcgacttc	780
caacaggcac tcgaacaaaa cgggcattat tccggcgcgt ccgtacaagc cgacttcgac	840
cgtctccaag gcgaccgcgt ccccgtaaaa gtcagcgtaa ccgaggtcaa acgccacaag	900
ctcgaaaccg gcatccgcct cgattcggaa tacggtttgg gcggcaaaat cgcttacgac	960
tattacaacc tcttcaacaa aggttatatc ggctcggtcg tctgggatat ggacaaatc	1020
gaaaccacgc ttgccgcgg catcagccag ccgcgcaact atcggggcaa ctactggaca	1080
agcaacgttt cctacaacgg ttcgaccacc caaaacctcg aaaaacgcgc cttctccggc	1140
ggcatctggg atgtgcgcga ccgcgcgggc atcgatgcca ggctgggggc agagtttctc	1200
gcagaaggcc ggaatatccc cggctcggat atcgatttgg gcaacagcca cgccacgatg	1260
ctgaccgcct cttggaaacg ccagctgctc aacaacgtgc tgcattccga aaacggccat	1320



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tacctcgacg gcaaaatcgg tacgactttg ggcacattcc tgtcctccac cgcgctgac 1380
cgcacctctg cccgtgcagg ttattttctt acgcccga aaacaaaaact cggcacgttc 1440
atcatacgcg gacaagcggg ttacaccgtt gcccgcgaca atgccgacgt tccttcaggg 1500
ctgatgttcc gcagcggcgg cgcgtcttcc gtgcgcgggt acgaactcga cagcatcgga 1560
cttgccggcc cgaacggatc ggtcctgccc gaacgcgccc tcctgggtggg cagcctggaa 1620
taccaactgc cgtttacgcg caccctttcc ggcgcggtgt tccacgatat gggcgatgcc 1680
gccgccaatt tcaaactgat gaagctgaaa cacggttcgg gactgggcgt gcgctggttc 1740
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tggcacatca gcttgggaac acgcttctaa 1830

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&lt;210&gt; 2

&lt;211&gt; 609

&lt;212&gt; PRT

<213> *Neisseria meningitidis*

&lt;400&gt; 2

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Met Met Ile Lys Pro Thr Ala Leu Leu Leu Pro Ala Leu Phe Phe Phe
  1             5             10             15
Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala
      20             25             30
Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys
      35             40             45
Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile
      50             55             60
Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu
      65             70             75             80
Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro
      85             90             95
Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys
      100            105            110
Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro
      115            120            125
Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp
      130            135            140
Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu
      145            150            155            160
Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu
      165            170            175
Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro
      180            185            190
Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala

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195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro  
 530 535 540  
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala  
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 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly  
 565 570 575  
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr  
 580 585 590  
 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg  
 595 600 605  
 Phe

&lt;210&gt; 3

&lt;211&gt; 1830

&lt;212&gt; DNA

<213> *Neisseria meningitidis*

&lt;400&gt; 3

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 taccaactgc cgtttacgcg caccctttcc ggcgcgggtg tccacgatat gggcgatgcc 1680  
 gccgccaatt tcaaactgat gaagctgaaa cacggttcgg gactgggcgt gcgctgggtc 1740  
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<210> 4

<211> 609

<212> PRT

<213> *Neisseria meningitidis*

<400> 4

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 Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys  
 35 40 45  
 Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile  
 50 55 60  
 Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu  
 65 70 75 80  
 Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro  
 85 90 95  
 Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys  
 100 105 110  
 Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro  
 115 120 125  
 Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp  
 130 135 140  
 Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu  
 145 150 155 160  
 Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu  
 165 170 175  
 Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro  
 180 185 190  
 Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala

195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro  
 530 535 540  
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala  
 545 550 555 560  
 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly  
 565 570 575  
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr  
 580 585 590  
 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg  
 595 600 605  
 Phe

&lt;210&gt; 5

&lt;211&gt; 1764

&lt;212&gt; DNA

<213> *Neisseria meningitidis*

&lt;400&gt; 5

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gcctcttggg	aacgccagct	gctcaacaac	gtgctgcac	ccgaaaacgg	ccattacctc	1260
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&lt;210&gt; 6

&lt;211&gt; 587

&lt;212&gt; PRT

<213> *Neisseria meningitidis*

&lt;400&gt; 6

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Asn Lys Ser Pro Asp Thr Glu Ser Val Lys Leu Lys Pro Lys Phe Pro
      20             25             30
Val Leu Ile Asp Thr Gln Asp Ser Glu Ile Lys Asp Met Val Glu Glu
      35             40             45
His Leu Pro Leu Ile Thr Gln Gln Gln Glu Glu Val Leu Asp Lys Glu
      50             55             60
Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro Asp Asn Val Lys Thr Met
65             70             75             80
Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys Val Ser Leu Thr Glu Lys
      85             90             95
Asp Gly Ala Tyr Thr Val His Ile Thr Pro Gly Pro Arg Thr Lys Ile
      100            105            110
Ala Asn Val Gly Val Ala Ile Leu Gly Asp Ile Leu Ser Asp Gly Asn
      115            120            125
Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu Asn Trp Gln Gln Pro Val
      130            135            140
Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu Asn Ser Lys Thr Ser Val
145            150            155            160
Leu Gly Ala Val Thr Arg Lys Ala Tyr Pro Leu Ala Lys Leu Gly Asn
      165            170            175
Thr Gln Ala Ala Val Asn Pro Asp Thr Ala Thr Ala Asp Leu Asn Val
      180            185            190
Val Val Asp Ser Gly Arg Pro Ile Ala Phe Gly Asp Phe Glu Ile Thr
      195            200            205

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Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val Ser Gly Leu Ala Arg Phe  
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 Gln Pro Gly Met Pro Tyr Asp Leu Asp Leu Leu Leu Asp Phe Gln Gln  
 225 230 235 240  
 Ala Leu Glu Gln Asn Gly His Tyr Ser Gly Ala Ser Val Gln Ala Asp  
 245 250 255  
 Phe Asp Arg Leu Gln Gly Asp Arg Val Pro Val Lys Val Ser Val Thr  
 260 265 270  
 Glu Val Lys Arg His Lys Leu Glu Thr Gly Ile Arg Leu Asp Ser Glu  
 275 280 285  
 Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp Tyr Tyr Asn Leu Phe Asn  
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 Lys Gly Tyr Ile Gly Ser Val Val Trp Asp Met Asp Lys Tyr Glu Thr  
 305 310 315 320  
 Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg Asn Tyr Arg Gly Asn Tyr  
 325 330 335  
 Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser Thr Thr Gln Asn Leu Glu  
 340 345 350  
 Lys Arg Ala Phe Ser Gly Gly Val Trp Tyr Val Arg Asp Arg Ala Gly  
 355 360 365  
 Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu Ala Glu Gly Arg Lys Ile  
 370 375 380  
 Pro Gly Ser Ala Val Asp Leu Gly Asn Ser His Ala Thr Met Leu Thr  
 385 390 395 400  
 Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn Val Leu His Pro Glu Asn  
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 Gly His Tyr Leu Asp Gly Lys Ile Gly Thr Thr Leu Gly Thr Phe Leu  
 420 425 430  
 Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala Arg Ala Gly Tyr Phe Phe  
 435 440 445  
 Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe Ile Ile Arg Gly Gln Ala  
 450 455 460  
 Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp Val Pro Ser Gly Leu Met  
 465 470 475 480  
 Phe Arg Ser Gly Gly Ala Ser Ser Val Arg Gly Tyr Glu Leu Asp Ser  
 485 490 495  
 Ile Gly Leu Ala Gly Pro Asn Gly Ser Val Leu Pro Glu Arg Ala Leu  
 500 505 510  
 Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro Phe Thr Arg Thr Leu Ser  
 515 520 525  
 Gly Ala Val Phe His Asp Met Gly Asp Ala Ala Ala Asn Phe Lys Arg



530                      535                      540  
 Met Lys Leu Lys His Gly Ser Gly Leu Gly Val Arg Trp Phe Ser Pro  
 545                      550                      555                      560  
 Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr Gly His Ser Asp Lys Lys  
                     565                      570                      575  
 Ile Arg Trp His Ile Ser Leu Gly Thr Arg Phe  
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<400> 8  
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<210> 9  
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 <213> Artificial Sequence

<220>  
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<400> 9  
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 <213> *Neisseria meningitidis*

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 agaatcgaac tctgccacac cgatgcacga caccgtacc 1000